

Thu Jan 24 07:40:21 2002

us-09-531-438-4.oli.rng

Page 1

GenCore version 4.5  
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ON nucleic - nucleic search, using sw model

Run on: January 24, 2002, 03:28:19 : Search time 222.28 Seconds

(without alignments)  
347.126 Million cell updates/sec

Title: US-09-531-438-4

Perfect score: 90

Sequence: 1 atgaaaaaattattcnaa.....gtccaatgaagcaagtga 90

Scoring table: OLIGO\_NUC  
Gapop 60.0, Capext 60.0

Searched: 930621 seqs, 428662619 residues

Word size: 0

Total number of hits satisfying chosen parameters: 989696

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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5: /SID52/gcgdata/geneseq/geneseq/NA1984.DAT.\*  
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21: /SID52/gcgdata/geneseq/geneseq/NA2000.DAT.\*  
22: /SID52/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	15.6	20	AA205048	PCR primer used to
2	14	15.6	26	AAV07952	Helicobacter pylori
3	14	15.6	26	AAV07952	Helicobacter pylori
4	14	15.6	27	AAV07937	Helicobacter pylori
5	14	15.6	47	AA268842	Human map-related
6	14	15.6	17	AA268842	Renilla reniformis
7	14	15.6	20	AA268842	PCR primer used to
8	14	15.6	23	AA268842	Human SCNA PCR-SS
9	14	15.6	24	AA268842	B. thuringiensis 33
10	14	15.6	26	AA268842	Alzheimer's diseases
11	14	15.6	26	AA268842	Alzheimer's diseases

12	13	14.4	26	21	AA267342	Alzheimer's diseases
13	13	14.4	31	19	AAV07957	Helicobacter pylori
14	13	14.4	34	16	AA215377	A2F ASF cosmid c10
15	13	14.4	35	22	AA261207	Coxsackie virus B
16	13	14.4	36	22	AA2690560	Dissociation trans
17	13	14.4	38	17	AA234130	III. promoter-RTV-
18	13	14.4	39	13	AA235630	HIV-2 env 3', fragm
19	13	14.4	39	14	AA235630	PCR primer HIV2B2.
20	13	14.4	39	14	AA235630	Plasmid pMycR PC
21	13	14.4	40	21	AA261322	Insecticidal prote
22	13	14.4	40	21	AA261322	Primer 3A used to
23	13	14.4	41	19	AA261323	Maize polymorphic
24	13	14.4	41	19	AA261323	Maize polymorphic
25	13	14.4	41	19	AA261323	Human gene signatu
26	13	14.4	50	16	AA250774	Synthetic plasmid
27	13	14.4	50	20	AA252184	Synthetic plasmid
28	13	14.4	50	20	AA252184	Human fli1 VBSF re
29	13	14.4	50	20	AA252184	Human fli1 VBSF re
30	13	14.4	50	20	AA252184	Human fli1 VBSF re
31	13	14.4	50	20	AA252184	Human fli1 VBSF re
32	13	14.4	50	20	AA252184	Human fli1 VBSF re
33	13	14.4	50	20	AA252184	Human fli1 VBSF re
34	13	14.4	50	20	AA252184	Human fli1 VBSF re
35	13	14.4	50	20	AA252184	Human fli1 VBSF re
36	13	14.4	50	20	AA252184	Human fli1 VBSF re
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44	13	14.4	50	20	AA252184	Human fli1 VBSF re
45	13	14.4	50	20	AA252184	Human fli1 VBSF re

#### ALIGNMENTS

RESULT 1	
AA205048	AA205048 standard; DNA: 20 BP.
AC	AA205048:
DT	07-OCT-1999 (first entry)
DE	PCR primer used to amplify an ORF of Chlamydia trachomatis.
KW	Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW	paratrachoma; inclusion conjunctivitis; genital disease; peritphalitis;
KW	nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
KW	bartholinitis; pneumonia; venereal lymphogranulomatosis; ss.
OS	Synthetic.
OS	Chlamydia trachomatis.
PM	W09928475-A2.
PD	10-JUN-1999.
PF	27-NOV-1998; 98NO-IB01939.
PR	04-NOV-1998; 98US-0107077.
PR	28-NOV-1997; 97ER-0015041.
PR	17-DEC-1997; 97ER-0016034.
PA	(GEST ) GENSET.
PI	Griffiths R;
PI	Griffiths R;
DR	WPI: 1999-371125/31.

PT Genome sequence of Chlamydia trachomatis  
 XX  
 PS Disclosure: Page 1738; 1755pp: English.  
 XX  
 CC PCR primers AA201426-206209 were used to amplify open reading frames  
 CC (ORFs) of the genome of Chlamydia trachomatis (see AA201425). These ORFs  
 CC encode polypeptides (see AA35754-Y37949) which can be used as vaccines  
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences  
 CC can also be used to control growth of the microorganism. Chlamydia  
 CC trachomatis is responsible for a large number of diseases, e.g. eye  
 CC diseases such as conventional trachoma, nonendemic trachoma,  
 CC paratrachoma, and inclusion conjunctivitis; genital diseases such as  
 CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,  
 CC peritonitis, Bartholinitis, pneumopathy in breast feeding infants;  
 CC and venereal lymphogranulomatosis. The polypeptides of the  
 CC invention may be of use in treating these diseases.  
 CC  
 SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 other;

Query Match 15.6%; Score 14; DB 20; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 54 ttttcttgagacaa 67  
 |||||  
 Db 4 ttttcttgagacaa 17

## RESULT 2

AAV07952/c  
 ID AAV07952 standard; DNA; 26 BP.

AAV07952:

02-FEB-1999 (first entry)

Helicobacter pylori polypeptide GHPO 1414 5' DNA primer.

GHPO 1414; infection; gastritis; ulcer; vaccine; diagnosis;  
 therapy; PCR; primer; ss.

Synthetic.  
 Helicobacter pylori.

MO9843479-A1.

08-OCT-1998.

31-MAR-1998; 98MO-US06421.

01-APR-1997; 97US-0834666.

01-APR-1997; 97US-0831310.

(HUMA-) HUMAN GENOME SCI INC.

(INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS ET VACCINS.

Al-Garawi A, Kleanthous H, Lissolo L, Miller C, Tomb J;

WPI; 1998-568251/48.

New isolated Helicobacter polynucleotides - used to develop products  
 for the diagnosis, prevention and treatment of Helicobacter  
 infections and gastroduodenal diseases

Claim 5; Page 145; 184pp: English.

This 5' primer is used with a 3' primer (see AAV07954) in the PCR  
 amplification of Helicobacter, e.g. Helicobacter pylori, genomic  
 DNA in order to obtain DNA (see AAV07921) encoding the unprocessed  
 form of a 76 kDa polypeptide (see AAV73032) designated GHPO 1414.  
 The isolated polynucleotide, and encoded polypeptide, can be used  
 to develop vaccines for the treatment and prevention of Helicobacter

CC Infections.  
 XX  
 SQ Sequence 26 BP; 14 A; 5 C; 4 G; 3 T; 0 other;

Query Match 15.6%; Score 14; DB 19; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 40 ttttctgtttct 53  
 |||||  
 Db 18 TTTTCATGTTTCT 5

## RESULT 3

AAV07922/c  
 ID AAV07922 standard; DNA; 26 BP.

AAV07922:

02-FEB-1999 (first entry)

Helicobacter pylori polypeptide GHPO 386 5' DNA primer.

GHPO 386; infection; gastritis; ulcer; vaccine; diagnosis; therapy;  
 PCR; primer; ss.

Synthetic.  
 Helicobacter pylori.

MO9843479-A1.

08-OCT-1998.

31-MAR-1998; 98MO-US06421.

01-APR-1997; 97US-0834666.

01-APR-1997; 97US-0831310.

(HUMA-) HUMAN GENOME SCI INC.

(INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS ET VACCINS.

Al-Garawi A, Kleanthous H, Lissolo L, Miller C, Tomb J;

WPI; 1998-568251/48.

New isolated Helicobacter polynucleotides - used to develop products  
 for the diagnosis, prevention and treatment of Helicobacter  
 infections and gastroduodenal diseases

Claim 5; Page 137; 184pp: English.

This 5' primer is used with a 3' primer (see AAV07924) in the PCR  
 amplification of Helicobacter, e.g. Helicobacter pylori, genomic  
 DNA in order to obtain DNA (see AAV72001  
 CC ) encoding the unprocessed  
 CC form of a 76 kDa polypeptide (see AAV73032) designated GHPO 386. The  
 CC isolated polynucleotide, and encoded polypeptide, can be used to  
 CC develop vaccines for the treatment and prevention of Helicobacter  
 CC infections.  
 CC

Sequence 26 BP; 15 A; 5 C; 4 G; 2 T; 0 other;

Query Match 15.6%; Score 14; DB 19; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 40 ttttctgtttct 53  
 |||||  
 Db 20 TTTTCATGTTTCT 7

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OM nucleic - nucleic search, using SW model

Run on: January 24, 2002, 02:22:33 : Search time 93.51 Seconds  
(without alignments)  
791.983 Million cell updates/sec

Title: US-09-531-438-3

Perfect score: 337  
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Scoring table: OLIGO-MUC  
Gapop 60.0, Gapext 60.0

Searched: 351203 seqs, 113238999 residues

Word size : 5 0

Total number of hits satisfying chosen parameters: 495388

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

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4: /cgn2\_6/ptodate/2/1na/6b\_COMB.seq: \*  
5: /cgn2\_6/ptodate/2/1na/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodate/2/1na/backfileal.seq: \*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	4.9	29	3 US-08-816-977-12	Sequence 12, Appl
2	16	4.9	36	1 US-08-639-600-16	Sequence 16, Appl
3	15	4.6	27	1 US-08-120-827-66	Sequence 66, Appl
4	15	4.6	27	1 US-08-478-675-66	Sequence 66, Appl
5	15	4.6	30	5 PCT-US92-10792-3	Sequence 3, Appl1
6	15	4.6	32	1 US-08-256-261-29	Sequence 29, Appl
7	15	4.6	32	3 US-08-852-299-29	Sequence 29, Appl
8	14	4.3	18	2 US-09-205-204-20	Sequence 20, Appl
9	14	4.3	29	3 US-08-816-977-12	Sequence 12, Appl
10	14	4.3	30	2 US-08-639-001A-31	Sequence 31, Appl
11	14	4.3	30	4 US-08-642-274D-110	Sequence 110, App
12	14	4.3	36	1 US-08-639-600-16	Sequence 16, Appl
13	14	4.3	37	2 US-08-403-853-8	Sequence 8, Appl1
14	14	4.0	18	3 US-08-847-844A-113	Sequence 113, App
15	14	4.0	18	4 US-08-686-968C-13	Sequence 13, Appl
16	14	4.0	20	3 US-09-288-461-79	Sequence 79, Appl
17	14	4.0	21	3 US-08-691-045-61	Sequence 61, Appl
18	14	4.0	24	3 US-08-672-115-1	Sequence 1, Appl1
19	14	4.0	28	1 US-08-120-827-64	Sequence 64, Appl
20	14	4.0	28	1 US-08-478-675-64	Sequence 64, Appl
21	14	4.0	30	2 US-08-642-274D-158	Sequence 79, Appl
22	14	4.0	30	4 US-08-639-001A-79	Sequence 158, App
23	13	4.0	31	1 US-08-310-638D-5	Sequence 5, Appl1
24	13	4.0	31	2 US-08-906-746A-5	Sequence 5, Appl1
25	13	4.0	36	1 US-08-247-809A-14	Sequence 14, Appl
26	13	4.0	36	2 US-08-711-728-14	Sequence 14, Appl
27	13	4.0	37	2 US-08-097-554A-45	Sequence 45, Appl

28	13	4.0	37	2 US-08-484-575A-10	Sequence 10, Appl
29	13	4.0	37	3 US-08-477-459-10	Sequence 10, Appl
30	13	4.0	37	3 US-08-480-640A-45	Sequence 45, Appl
31	13	4.0	37	3 US-08-479-869-10	Sequence 10, Appl
32	13	4.0	37	3 US-08-295-802-45	Sequence 45, Appl
33	13	4.0	37	3 US-08-486-414-10	Sequence 10, Appl
34	13	4.0	37	4 US-08-488-237A-45	Sequence 45, Appl
35	13	4.0	37	5 PCT-US94-01826A-10	Sequence 10, Appl
36	13	4.0	37	5 PCT-US94-02252A-10	Sequence 10, Appl
37	13	4.0	38	5 PCT-US96-00547-40	Sequence 40, Appl
38	13	4.0	39	1 US-08-105-483-168	Sequence 168, App
39	13	4.0	39	1 US-08-709-209-168	Sequence 168, App
40	13	4.0	39	1 US-08-303-275-56	Sequence 56, Appl
41	13	4.0	39	1 US-08-458-101-168	Sequence 168, App
42	13	4.0	39	2 US-09-028-361A-19	Sequence 19, Appl
43	13	4.0	40	1 US-08-199-507B-39	Sequence 39, Appl
44	13	4.0	40	1 US-08-441-828-39	Sequence 39, Appl
45	13	4.0	41	3 US-08-930-503A-11	Sequence 11, Appl

#### ALIGNMENTS

RESULT 1  
US-08-816-977-12  
Sequence 12, Application US/08816977  
Patient No. 6080400  
GENERAL INFORMATION:  
APPLICANT: Williams, James A.  
APPLICANT: Byrne, Lisa M.  
TITLE OF INVENTION: Prevention And Treatment Of  
TITLE OF INVENTION: Verotoxin-Induced Disease  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medien & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/816,977  
FILING DATE: 13-MAR-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamlin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: OPHD-02450  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-816-977-12

Query Match 4.9%: Score 16: DB 3: Length 29:

Best Local Similarity 100.0%: Pred. No. 3.1e+02: 0: Gaps 0:

Matches 16: Conservative 0: Mismatches 0: Indels 0:

189 aaataatcattccta 204

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DB 9 AAAAAAAAAATTTT 24

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RESULT 2
US-08-629-600-16
Sequence 16, Application US/08629600
Patent No. 5783196
GENERAL INFORMATION:
APPLICANT: NORIEGA, Fernando
APPLICANT: LEVINE, Myron M.
TITLE OF INVENTION: GUA MUTANTS OF SHIGELLA
TITLE OF INVENTION: AND VACCINES CONTAINING THE SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MIOM, 21NN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
CITY: Washington, D.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/629,600
FILING DATE: 9-APR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KIT, Gordon
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-6765
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
US-08-629-600-16

Query Match 4.9%; Score 16; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 189 aaaaattttttttt 204
DB 14 AAAAAAAAAATTTT 29

RESULT 3
US-08-120-827-66
Sequence 66, Application US/08120827
Patent No. 5525495
GENERAL INFORMATION:
APPLICANT: KEENE, JACK D.
APPLICANT: KING, PETER H.
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE
TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF
TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1735 Jefferson Davis Highway, Fourth Floor
CITY: Arlington

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STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/120,827
FILING DATE: 15-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5525495man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 714-158-0 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPRT UR
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: RNA (genomic)
US-08-120-827-66

Query Match 4.6%; Score 15; DB 1; Length 27;
Best Local Similarity 33.3%; Pred. No. 7.9e+02;
Matches 5; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

OY 197 tatttttttttaa 211
DB 12 UUUUUUUUUUUAAA 26

RESULT 4
US-08-478-675-66
Sequence 66, Application US/08478675
Patent No. 5773246
GENERAL INFORMATION:
APPLICANT: KEENE, JACK D.
APPLICANT: KING, PETER H.
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE
TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS
TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1735 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,675
FILING DATE: 07-JUN-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/120,827
FILING DATE: 15-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5773246man F.

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 24, 2002, 02:19:03 : Search time 1494.92 Seconds

(without alignments)  
3608.606 Million cell updates/sec

Title: US-09-531-438-3

Perfect score: 327

Sequence: 1 attcgagatatttaattt.....tttcatttttttttttgc 327

Scoring table: OLIGO\_NUC  
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Searched: 1472140 seqs, 824858955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 541028

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : GenBank:  
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2: gb\_hg:\*  
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11: gb\_sc:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_da:\*  
16: em\_fun:\*  
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27: em\_sy:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htgo\_hum:\*  
31: em\_htgo\_in:\*  
32: em\_htgo\_ro:\*  
33: em\_htgo\_hum:\*  
34: em\_htgo\_in:\*  
35: em\_htgo\_ro:\*  
36: em\_htg\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	4.9	29	6	AR099868
2	32	4.9	32	6	E27913
3	16	4.9	36	3	CEANONYFR
4	16	4.9	36	6	AR019036
5	15	4.6	27	6	AR014030
6	15	4.6	27	6	I21980
7	15	4.6	32	6	AR037189
8	15	4.3	18	6	AR076353
9	10	4.3	29	6	AR099868
10	11	4.3	30	6	AR028182
11	14	4.3	32	6	E27913
12	14	4.3	36	6	AR019036
13	14	4.3	37	6	AR063204
14	14	4.3	45	6	AR049873
15	14	4.3	45	6	AR049874
16	14	4.3	45	6	AR099855
17	14	4.3	45	6	AR099856
18	14	4.3	45	6	AX137975
19	14	4.3	45	6	AX137976
20	14	4.3	50	6	AX159856
21	14	4.3	50	6	AR146953
22	13	4.0	20	6	AR121058
23	13	4.0	23	6	AR076045
24	13	4.0	23	6	AR076045
25	13	4.0	23	6	AR076045
26	13	4.0	24	6	AR093544
27	13	4.0	24	6	AX164353
28	13	4.0	24	12	AB069100
29	13	4.0	25	6	AX042574
30	13	4.0	25	6	AX043268
31	13	4.0	26	6	AX039624
32	13	4.0	26	6	AX039624
33	13	4.0	28	6	AR014028
34	13	4.0	28	6	I21978
35	13	4.0	29	6	AR012366
36	13	4.0	29	6	E59972
37	13	4.0	30	6	AR028230
38	13	4.0	30	6	AR138633
39	13	4.0	30	6	AX063379
40	13	4.0	31	6	I95122
41	13	4.0	33	5	XELARE59
42	13	4.0	36	6	AA1027
43	13	4.0	36	6	AR082586
44	13	4.0	36	6	AX157671
45	13	4.0	36	6	I28261

## ALIGNMENTS

RESULT	1	LOCUS	AR099868	SEQUENCE	29 bp	DNA	PAT	14-FEB-2001
DEFINITION	AR099868	Sequence	12 from patent US 6080400.					
ACCESSION	AR099868	Sequence	12 from patent US 6080400.					
VERSION	AR099868.1	GI:12810316						
KEYWORDS	Unknown.							
SOURCE	Unknown.							
ORGANISM	Unknown.							
REFERENCE	1 (bases 1 to 29)							
AUTHORS	Williams, J.A. and Byrne, L.Marie.							
TITLE	Compositions for the prevention and treatment of verotoxin-induced disease							
JOURNAL	Patent: US 6080400-A							
FEATURES	Location/Qualifiers							
BASE COUNT	11 a 29							
ORIGIN	11 a 29							

JOURNAL and Immunoregulation  
Patent: US 5773246-A 66 30-JUN-1998;  
FEATURES Location/Qualifiers  
SOURCE 1..27  
/organism="unknown"  
BASE COUNT 7 a 2 c 2 g 16 t  
ORIGIN

Query Match 4.6%; Score 15; DB 6; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.4e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 197 tattttatttttaa 211  
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Db 12 TATTTTATTTTAA 26

RESULT 6  
LOCUS 121980 27 bp DNA PAT 07-OCT-1996  
DEFINITION Sequence 66 from patent US 5525495.  
ACCESSION 121980  
VERSION 121980.1 GI:1602334  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 27)  
AUTHORS Keene,J.D., Levine,T. and Gao,F.  
TITLE Methods and compositions useful in the recognition, binding and expression of ribonucleic acids involved in cell growth, neoplasia and immunoregulation  
JOURNAL Patent: US 5525495-A 66 11-JUN-1996;  
FEATURES Location/Qualifiers  
SOURCE 1..27  
/organism="unknown"

BASE COUNT 7 a 2 c 2 g 16 t  
ORIGIN

Query Match 4.6%; Score 15; DB 6; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.4e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 197 tattttatttttaa 211  
|||||  
Db 12 TATTTTATTTTAA 26

RESULT 7  
LOCUS AR037189 32 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 29 from patent US 5801037.  
ACCESSION AR037189  
VERSION AR037189.1 GI:5955045  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 32)  
AUTHORS Behnke,D., Schlotz,B., Albrecht,S., Guhrs,K. and Hartmann,M.  
TITLE Expression of signal-peptide-free staphylokinases  
JOURNAL Patent: US 5801037-A 29 01-SEP-1998;  
FEATURES Location/Qualifiers  
SOURCE 1..32  
/organism="unknown"

BASE COUNT 3 a 8 c 4 g 17 t  
ORIGIN

Query Match 4.6%; Score 15; DB 6; Length 32;  
Best Local Similarity 100.0%; Pred. No. 2.4e+04;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 154 aaaggaataataa 168  
|||||  
Db 30 AAAGGAATAATAA 16

RESULT 8  
LOCUS AR076353 18 bp DNA PAT 30-AUG-2000  
DEFINITION Sequence 20 from patent US 5958772.  
ACCESSION AR076353  
VERSION AR076353.1 GI:10003099  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)  
AUTHORS Bennett,C.Frank, Ackermann,E.J. and Cosset,L.M.  
TITLE Antisense inhibition of cellular inhibitor of apoptosis-1 expression  
JOURNAL Patent: US 5958772-A 20 28-SEP-1999;  
FEATURES Location/Qualifiers  
SOURCE 1..18  
/organism="unknown"

BASE COUNT 3 a 2 c 1 g 12 t  
ORIGIN

Query Match 4.3%; Score 14; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.2e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 160 aaataataataa 173  
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Db 18 AAATAATAATAA 5

RESULT 9  
LOCUS AR099868 29 bp DNA PAT 14-FEB-2001  
DEFINITION Sequence 12 from patent US 6080400.  
ACCESSION AR099868  
VERSION AR099868.1 GI:12810316  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 29)  
AUTHORS Williams,J.A. and Byrne,L.Marie.  
TITLE Compositions for the prevention and treatment of verotoxin-induced disease  
JOURNAL Patent: US 6080400-A 12 27-JUN-2000;  
FEATURES Location/Qualifiers  
SOURCE 1..29  
/organism="unknown"

BASE COUNT 11 a 2 c 5 g 11 t  
ORIGIN

Query Match 4.3%; Score 14; DB 6; Length 29;  
Best Local Similarity 100.0%; Pred. No. 6.1e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 189 aaataatttttt 202  
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Db 22 AAATAATTATTTT 9

RESULT 10  
LOCUS AR028182 30 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 31 from patent US 5858661.

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 24, 2002, 01:12:37 : Search time 1502.85 Seconds

(without alignments)  
3589.565 Million cell updates/sec

Title: US-09-531-438-3

Perfect score: 327  
Sequence: 1 attggagatacttaatt.....tttcattttcttatgtgt 327

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank :  
1: gb\_ba :  
2: gb\_hg :  
3: gb\_in :  
4: gb\_om :  
5: gb\_ov :  
6: gb\_ph :  
7: gb\_pl :  
8: gb\_pr :  
9: gb\_ro :  
10: gb\_ro :  
11: gb\_ro :  
12: gb\_ro :  
13: gb\_un :  
14: gb\_vl :  
15: en\_ba :  
16: en\_fun :  
17: en\_hum :  
18: en\_in :  
19: en\_om :  
20: en\_om :  
21: en\_ov :  
22: en\_pat :  
23: en\_ph :  
24: en\_pl :  
25: en\_ro :  
26: en\_ro :  
27: en\_ro :  
28: en\_ro :  
29: en\_vl :  
30: en\_hgo\_hum :  
31: en\_hgo\_hum :  
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39: en\_hgo\_hum :  
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42: en\_hgo\_hum :  
43: en\_hgo\_hum :  
44: en\_hgo\_hum :  
45: en\_hgo\_hum :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	327	100.0	327	6	AX004614
2	327	100.0	1392	1	L77965
3	327	100.0	1392	6	AX004613
4	199	60.9	54310	1	AP003515
5	81.8	25.0	12900	3	AF001429
6	77.8	24.2	39347	9	AL135906
7	77.8	23.8	53932	2	AC023371
8	77.4	23.7	163443	2	AC006280
9	77.4	23.7	205429	2	AC005506
10	76.2	23.3	3392	3	AF300334
11	76.2	23.3	242513	2	AC079314
12	75.8	23.2	318221	2	PFMAL13P3
13	75.6	23.1	140414	2	AF377947
14	75	22.9	178783	9	AC068139
15	74.4	22.8	156050	2	AC004153
16	73.2	22.4	863	11	CNS06EVO
17	73.2	22.3	862	8	YSCWCTOC
18	72.8	22.3	34119	8	AF222718
19	72.2	22.1	104932	2	AC005504
20	72.2	22.1	162445	2	AL158151
21	72.2	22.1	169546	2	AC004157
22	72.2	22.1	159882	9	AL354720
23	72.2	22.0	158398	2	AC011146
24	71.6	21.9	180903	9	AC073409
25	71.4	21.8	12029	3	AB001400
26	71.4	21.8	175053	2	AC090014
27	71.2	21.8	110000	2	AL591074_2
28	71.2	21.7	95477	2	AC007076
29	71.1	21.7	168799	9	AC009531
30	71.1	21.7	194038	9	AC010103
31	70.8	21.6	159475	2	AC021378
32	70.6	21.6	13433	3	AF315648
33	70.6	21.6	85779	8	SC0011856
34	70.6	21.6	122747	2	AC093220
35	70.6	21.6	159255	2	AF212831
36	70.6	21.6	161230	2	AC011355
37	70.6	21.6	234112	3	PFMAL4P2
38	70.6	21.6	340000	9	HS21C013
39	70.4	21.5	155456	2	AC027753
40	70.4	21.5	160624	9	AC060835
41	70.4	21.5	172758	2	AC022553
42	70.4	21.5	199551	2	AC006281
43	70.2	21.5	137342	9	AL392048
44	70.2	21.5	180388	9	HDMREBLAS
45	70.2	21.5	183384	9	AC012492

## ALIGNMENTS

RESULT 1  
AX004614  
LOCUS AX004614 327 bp DNA  
DEFINITION Sequence 2 from Patent WO9915569.  
ACCESSION AX004614  
VERSION AX004614.1 GI:9928055  
KEYWORDS  
SOURCE  
ORGANISM  
Clostridium perfringens.  
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae; Clostridium.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
GIBERT M, and Popoff, M.R.  
Clostridium toxin, and method for preparing immunogenic compositions  
PATENT: WO 9915569-A 2 01-APR-1999;  
GIBERT M, and Popoff, M.R.  
Location/Qualifiers  
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# SUMMARIES

BASE COUNT 141 a /db\_xref="taxon:1502"  
ORIGIN 13 c 44 g 129 t

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Best Local Similarity 100.0% Pred. No. 3.5e-28;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 attggatcctcctaaatttagcacgaagaatgcttcaatgaatcaatcaaaa 60  
DB 1 ATTGGATCTCTTAATTAGCACGAAGAATGTTAAATGAATTAAGATTAATAA 60  
QY 61 gatactaatcatalagctgaagaattcaatcatalagatagctcaataaaa 120  
DB 61 GATATATTATATATAGCGAATAATTATATATATATATATATATATATATA 120  
QY 121 aaagtgctcgggggacacttttctttaaagaagaataataaatttagat 180  
DB 121 AAAGTGCTCGGGGACACTTTTGTGTTTAAAGAAATATATATATATATATAT 180  
QY 181 aaagtgcaaatcaattcttcttcaaatctgtaaaattgataaattgactg 240  
DB 181 AAAGTGCAATCAATCTCTTCTCAAAATTTGATATATATATATATATATAT 240  
QY 241 caaaaaaattcagggggaataataaataaataattcctcaagcttcaatc 300  
DB 241 TAAAAAAATTTACGGGGGAATATATGAATAAATTAATTTCAAGTTTACTGTAAT 300  
QY 301 ttatgtcttcacgttcttcttcttcttcttcttcttcttcttcttcttct 327  
DB 301 TTATGTTTCATGTTTCTTATGTTT 327

RESULT 2  
L77965 1392 bp DNA BCT 28-JUL-1998  
LOCUS Clostridium perfringens C beta 2 toxin gene, complete cds.  
DEFINITION L77965  
ACCESSION L77965  
VERSION L77965.1 GI:3342214  
KEYWORDS  
SOURCE Clostridium perfringens C.  
ORGANISM Clostridium perfringens C.  
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;  
Clostridium.

REFERENCE 1 (bases 1 to 1392)  
AUTHORS Gilbert M., Jolivet-Reynaud, C. and Popoff, M.R.  
TITLE Beta2 toxin, a novel toxin produced by Clostridium perfringens  
JOURNAL Gene 203 (1), 65-73 (1997)  
COMMENT 98085977  
REMARK Erratum: [[published erratum appears in Gene 1998 Mar 27:210(1):173]]

REFERENCE 2 (bases 1 to 1392)  
AUTHORS Popoff, M.R.  
TITLE Direct Submission  
JOURNAL Submitted (15-JAN-1998) Toxines Microbiennes, Institut Pasteur,  
Paris cedex 15 75724, France  
COMMENT GSDS:S:76036.  
FEATURES  
source location/Qualifiers  
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/note="putative"  
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CDS /codon\_start=1  
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/protein\_id="AAC27654.1"  
/db\_xref="GI:3342215"  
/translation="MKKIKSFYVIFMFSCFLIVGAIAPMKASAKRIDAVRKWENYL  
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NKTREPLNGALYDMFTVSSKDKLIVSDMEFTVNGKRYILTPSRVQVCHWDEL  
NOATGCVYRPTVSDRETYVADNMLNFRQATSSGRDIAKVSYSVVDHMKKDDVKASO  
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BASE COUNT 606 a 115 c 209 g 462 t  
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Query Match 100.0% Score 327; DB 1; Length 1392;  
Best Local Similarity 100.0% Pred. No. 2.8e-28;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATTGGATCTCTTAATTAGCACGAAGAATGTTAAATGAATTAAGATTAATAA 60  
QY 61 gatactaatcatalagctgaagaattcaatcatalagatagctcaataaaa 120  
DB 61 GATATATTATATATAGCGAATAATTATATATATATATATATATATATATA 120  
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DB 121 AAAGTGCTCGGGGACACTTTTGTGTTTAAAGAAATATATATATATATATAT 180  
QY 181 aaagtgcaaatcaattcttcttcaaatctgtaaaattgataaattgactg 240  
DB 181 AAAGTGCAATCAATCTCTTCTCAAAATTTGATATATATATATATATATAT 240  
QY 241 caaaaaaattcagggggaataataaataaataattcctcaagcttcaatc 300  
DB 241 TAAAAAAATTTACGGGGGAATATATGAATAAATTAATTTCAAGTTTACTGTAAT 300  
QY 301 ttatgtcttcacgttcttcttcttcttcttcttcttcttcttcttcttct 327  
DB 301 TTATGTTTCATGTTTCTTATGTTT 327

RESULT 3  
AX004613 1392 bp DNA PAT 24-AUG-2000  
LOCUS AX004613  
DEFINITION Sequence 1 from Patent WO915669.  
ACCESSION AX004613  
VERSION AX004613.1 GI:9928053  
KEYWORDS  
SOURCE Clostridium perfringens.  
ORGANISM Clostridium perfringens.  
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;  
Clostridium.

REFERENCE 1 (bases 1 to 1392)  
AUTHORS Gilbert M. and Popoff, M.R.  
TITLE Clostridium toxin, and method for preparing immunogenic  
JOURNAL compositions  
COMMENT Patent: WO 915669-A 1 01-APR-1999;  
GIBERT MARISE (FR); PASTEUR INSTITUT (FR)  
FEATURES  
source location/Qualifiers  
1..1392

/organism="Clostridium perfringens"  
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268..1065  
/note="unnamed protein product"  
CDS /codon\_start=1  
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/db\_xref="GI:9928054"  
/translation="MKKIKSFYVIFMFSCFLIVGAIAPMKASAKRIDAVRKWENYL"